

on objective clinical criteria (i.e., presence of systemic and local signs of infection and use of antifungals for  $\geq 10$  days) or non-IFI wounds if they failed to meet clinical criteria.

**Results.** Of 1932 subjects, 246 (12.7%) had laboratory evidence of fungal infection. There were a total of 143 IFI wounds ( $n = 94$ ), 157 non-IFI wounds ( $n = 96$ ), and 113 high suspicion wounds ( $n = 56$ ). IFI subjects had significantly higher injury severity scores (ISS median: 39.5 vs. 33), Sequential Organ Failure Assessment (SOFA) scores (7 vs. 2) and were more likely to require mechanical ventilation (66 vs. 28%). IFI patients also had higher ISS (93 vs. 84% with ISS  $> 25$ ) and SOFA scores (7 vs. 4) compared with the subjects with high suspicion wounds. IFI wounds often grew molds belonging to the order *Mucorales* compared with high suspicion (19 vs. 10%,  $P = 0.04$ ) and non-IFI wounds (19 vs. 7%,  $P = 0.02$ ). About half of the IF wounds grew fungi of the order *Mucorales* either isolated alone or in conjunction with other fungi, in comparison, 25% of the high suspicion wounds and 11% of the non-IFI wounds grew fungi of the order *Mucorales*. Three groups of fungi belonging to the order *Mucorales*, genus *Aspergillus* and *Fusarium* accounted for 83% of the IFI wounds and 74% of the high suspicion wounds.

**Conclusion.** Laboratory evidence of fungal infection is common among combat casualties. Clinical characteristics and wound microbiology allows us to group subjects into groups at low and high risk of IFI. Fungi of the order *Mucorales*, genus *Aspergillus* and *Fusarium* should not be considered contaminants. The presence of these fungi should obligate close clinical follow-up and debridement as needed.

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## 90. Increasing *Kingella* Identification in Bone and Joint Infections in Young Children

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**Session:** 30. It's not just Bones: Skin and Bones

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**Background.** *Kingella kingae* is an increasingly recognized pathogen among young children with bone and joint infections. Antibiotics given to cover methicillin-resistant *Staphylococcus aureus* are not effective against *Kingella*, and necessitate additional empiric antibiotics in this age group. Improving *Kingella* identification can narrow antibiotic choices and improve efficacy for long-term oral therapy.

**Methods.** We implemented a bone and joint infection guideline at a free standing children's hospital that called for early imaging, focal sampling, and polymerase chain reaction (PCR) testing for culture-negative specimens. The goal was to increase identification of *Kingella* and other pathogens to improve targeted antimicrobial therapy. Children 6 to  $\leq 60$  months of age with uncomplicated acute hematogenous osteomyelitis or septic arthritis between January 1, 2009–December 31, 2016, were included in this study. Outcomes of bacterial identification were measured.

**Results.** Charts for 49 cases that met criteria were reviewed. Prior to the algorithm, we identified *Kingella* in 4% (1/25) of cases. Following routine use of updated sampling and testing techniques, including PCR testing, *Kingella kingae* identification increased to 29% of cases (7/24;  $P = 0.02$ ) and, in fact, was the predominant pathogen identified in this age group.

**Conclusion.** Identification of *Kingella* was enhanced as a result of changes to sampling and testing, including PCR testing (Figure 1). Post-implementation, *Kingella* was more commonly identified than *Staphylococcus aureus*. Widespread availability of PCR testing in the future may allow for the use of narrowed antibiotic therapy and targeted transition to oral antibiotics in young children with bone or joint infection.

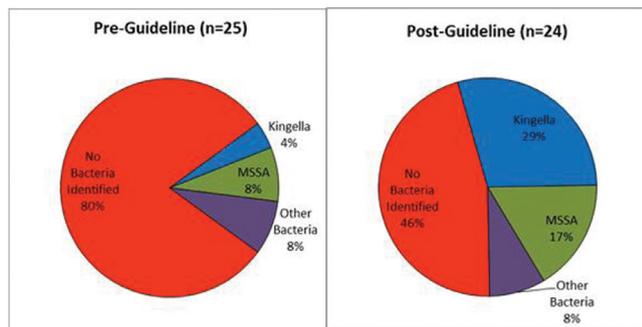


Figure 1. Bacterial identification pre and post guideline among children aged 6–60 months.

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## 91. Microbiology of Vertebral Osteomyelitis and Implications on Empiric Therapy

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**Background.** The management of vertebral osteomyelitis (VO) includes empiric antibiotic therapy while clinical cultures are being processed. Optimal antimicrobial therapy for VO, particularly when Gram-negative (GN) organisms are involved, is an area of ongoing debate. Narrow spectrum and oral antimicrobial therapy are preferred. The objective of this study was to identify characteristics of local pathogens and to formulate an institution-specific antibiotic protocol for empiric treatment of VO.

**Methods.** We conducted a retrospective case series study of adults diagnosed with VO from August 1, 2010 to August 31, 2015 at Palmetto Health Hospitals in Columbia, South Carolina. Cases identified by ICD-9 codes were included in the analysis if they met clinical, imaging and microbiology criteria.

**Results.** Analysis is based on 150 cases of VO with a mean age of 61 years, a male predominance (91; 61%), and an average body mass index of 29kg/m<sup>2</sup>. Comorbidities included diabetes mellitus (69; 46%), tobacco use (33; 22%), and hemodialysis (20; 13%). Thirty-seven (25%) cases had recent related injury or vertebral surgery, and 14 (9%) had prior hardware. Bone, disc, or adjacent tissue cultures were obtained in 129 (86%) of cases; 60 (40%) of these had  $> 1$  sample taken. The remaining 14% had blood cultures alone. Thirty-six cases (24%) had culture negative VO. In the remaining 114 cases, 132 organisms were isolated. A total of 111 (84%) organisms were Gram-positive cocci (GPC). Of those, the majority was *Staphylococcus aureus*. (66; 59%) (26/66 were methicillin-resistant), coagulase-negative staphylococci (20; 18%) and *Streptococcus* spp. (17; 15%). *Enterobacteriaceae* accounted for 13/17 Gram-negative bacilli (GNB), with only one isolate of *Pseudomonas aeruginosa*. Of the GNB, 11/17 were susceptible to either ceftriaxone or ciprofloxacin.

**Conclusion.** There was a predominance of VO due to GPC suggesting that intravenous vancomycin monotherapy may be reasonable for empiric therapy in noncritically ill patients while awaiting Gram stain and clinical culture results. Addition of either ceftriaxone or ciprofloxacin to vancomycin would increase cumulative antimicrobial coverage from 84 to 92%.

**Disclosures.** All authors: No reported disclosures.

## 92. Concordance of Results of Blood and Tissue Cultures from Patients with Pyogenic Spondylitis

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**Background.** The aim of this study was to investigate the concordance of results of blood and tissue cultures in patients with pyogenic spondylitis.

**Methods.** We searched the patients with pyogenic spondylitis in whom micro-organisms were isolated from both blood and tissue cultures by retrospective review of medical records in three tertiary university-affiliated hospitals between January 2005 and December 2015. The species and antimicrobial susceptibility patterns of isolates from blood and tissue cultures were compared with each other.

**Results.** Among 141 patients with pyogenic spondylitis in whom micro-organisms were isolated from both blood and tissue cultures, the species of blood and tissue isolates were identical in 135 patients (95.7%, 135/141). Excluding the four anaerobic isolates, we investigated antimicrobial susceptibility patterns of 131 isolates of same species from blood and tissue cultures. Antibiotic susceptibility patterns were identical in 128 patients (97.7%, 128/131). The most common isolates were *Staphylococcus aureus* (86 patients; 85 concordant and 1 discordant), followed by streptococcus (24 patients; 22 concordant and 2 discordant), and *Escherichia coli* (8 patients; all concordant).

**Conclusion.** We suggest that a positive blood culture from patients with pyogenic spondylitis could preclude the need for additional tissue cultures, especially when *S. aureus* and streptococcus grew in blood cultures.

Table 1. Micro-organisms isolated from blood and tissues in 135 patients with pyogenic spondylitis

Concordant (n = 135)	
<i>Staphylococcus aureus</i>	85
Viridans streptococci	11
<i>Streptococcus agalactiae</i>	8
<i>Escherichia coli</i>	8
<i>Enterococcus fecalis</i>	4
<i>Klebsiella pneumoniae</i>	2
Others	17
Discordant (n = 6)	
Blood	Tissue
<i>Propionibacterium avidum</i>	Coagulase-negative staphylococcus
<i>Streptococcus constellatus</i> ,	<i>Streptococcus constellatus</i> ,
<i>Actinomyces meyeri</i>	<i>Porphyromonas asaccharolytica</i>
<i>Staphylococcus epidermidis</i> , viridans	<i>Staphylococcus epidermidis</i>
streptococcus	
<i>Staphylococcus aureus</i>	<i>Staphylococcus aureus</i> , Nontuberculous mycobacteria